

Wim Van Criekinge

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

2,673
citations

236925

25
h-index

254184

43
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48
all docs

48
docs citations

48
times ranked

5073
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of DNA methylation in cancer: location revisited. <i>Nature Reviews Clinical Oncology</i> , 2018, 15, 459-466.	27.6	486
2	Detection of High-grade Prostate Cancer Using a Urinary Molecular Biomarker-based Risk Score. <i>European Urology</i> , 2016, 70, 740-748.	1.9	292
3	MEXPRESS: visualizing expression, DNA methylation and clinical TCGA data. <i>BMC Genomics</i> , 2015, 16, 636.	2.8	257
4	Transcriptional reprogramming by root knot and migratory nematode infection in rice. <i>New Phytologist</i> , 2012, 196, 887-900.	7.3	157
5	An update on sORFs.org: a repository of small ORFs identified by ribosome profiling. <i>Nucleic Acids Research</i> , 2018, 46, D497-D502.	14.5	135
6	PROTEOFORMER: deep proteome coverage through ribosome profiling and MS integration. <i>Nucleic Acids Research</i> , 2015, 43, e29-e29.	14.5	132
7	<i>MGMT</i> Promoter Methylation Cutoff with Safety Margin for Selecting Glioblastoma Patients into Trials Omitting Temozolomide: A Pooled Analysis of Four Clinical Trials. <i>Clinical Cancer Research</i> , 2019, 25, 1809-1816.	7.0	94
8	Food-derived opioid peptides inhibit cysteine uptake with redox and epigenetic consequences. <i>Journal of Nutritional Biochemistry</i> , 2014, 25, 1011-1018.	4.2	85
9	My-Forensic-Loci-queries (MyFLq) framework for analysis of forensic STR data generated by massive parallel sequencing. <i>Forensic Science International: Genetics</i> , 2014, 9, 1-8.	3.1	75
10	Risk score predicts high-grade prostate cancer in DNA-methylation positive, histopathologically negative biopsies. <i>Prostate</i> , 2016, 76, 1078-1087.	2.3	74
11	Genome-wide DNA Methylation Profiling Reveals Methylation Markers Associated with 3q Gain for Detection of Cervical Precancer and Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 3813-3822.	7.0	68
12	A urinary biomarker-based risk score correlates with multiparametric MRI for prostate cancer detection. <i>Prostate</i> , 2017, 77, 1401-1407.	2.3	61
13	Bacterial Diversity Assessment in Antarctic Terrestrial and Aquatic Microbial Mats: A Comparison between Bidirectional Pyrosequencing and Cultivation. <i>PLoS ONE</i> , 2014, 9, e97564.	2.5	60
14	Differential analysis of genome-wide methylation and gene expression in mesenchymal stem cells of patients with fractures and osteoarthritis. <i>Epigenetics</i> , 2017, 12, 113-122.	2.7	60
15	A Four-Gene Promoter Methylation Marker Panel Consisting of <i>GREM1</i> , <i>NEURL</i> , <i>LAD1</i> , and <i>NEFH</i> Predicts Survival of Clear Cell Renal Cell Cancer Patients. <i>Clinical Cancer Research</i> , 2017, 23, 2006-2018.	7.0	51
16	Cost-effectiveness of SelectMDx for prostate cancer in four European countries: a comparative modeling study. <i>Prostate Cancer and Prostatic Diseases</i> , 2019, 22, 101-109.	3.9	51
17	Cost-effectiveness of a new urinary biomarker-based risk score compared to standard of care in prostate cancer diagnostics – a decision analytical model. <i>BJU International</i> , 2017, 120, 659-665.	2.5	45
18	Methylome analysis of extreme chemoresponsive patients identifies novel markers of platinum sensitivity in high-grade serous ovarian cancer. <i>BMC Medicine</i> , 2017, 15, 116.	5.5	44

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19	PROTEOFORMER 2.0: Further Developments in the Ribosome Profiling-assisted Proteogenomic Hunt for New Proteoforms. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S126-S140.	3.8	43
20	Epigenetic markers in circulating cell-free DNA as prognostic markers for survival of castration-resistant prostate cancer patients. <i>Prostate</i> , 2018, 78, 336-342.	2.3	41
21	Methylation-mediated repression of PRDM14 contributes to apoptosis evasion in HPV-positive cancers. <i>Carcinogenesis</i> , 2014, 35, 2611-2618.	2.8	35
22	Spectral Prediction Features as a Solution for the Search Space Size Problem in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100076.	3.8	31
23	Identification and validation of <i>WISP1</i> as an epigenetic regulator of metastasis in oral squamous cell carcinoma. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 45-59.	2.8	28
24	Molecular and epigenetic features of melanomas and tumor immune microenvironment linked to durable remission to ipilimumab-based immunotherapy in metastatic patients. <i>Journal of Translational Medicine</i> , 2016, 14, 232.	4.4	27
25	BMP-SMAD Signaling Regulates Lineage Priming, but Is Dispensable for Self-Renewal in Mouse Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2016, 6, 85-94.	4.8	27
26	Evaluation of an Epigenetic Assay for Predicting Repeat Prostate Biopsy Outcome in African American Men. <i>Urology</i> , 2019, 128, 62-65.	1.0	24
27	On Cross-Sectional Associations of Leukocyte Telomere Length with Cardiac Systolic, Diastolic and Vascular Function: The Asklepios Study. <i>PLoS ONE</i> , 2014, 9, e115071.	2.5	19
28	Genome-wide DNA methylation detection by MethylCap-seq and Infinium HumanMethylation450 BeadChips: an independent large-scale comparison. <i>Scientific Reports</i> , 2015, 5, 15375.	3.3	17
29	Integrated transcriptomic and epigenomic analysis of ovarian cancer reveals epigenetically silenced GULP1. <i>Cancer Letters</i> , 2018, 433, 242-251.	7.2	16
30	Genome-wide methylome analysis using MethylCap-seq uncovers 4 hypermethylated markers with high sensitivity for both adeno- and squamous-cell cervical carcinoma. <i>Oncotarget</i> , 2016, 7, 80735-80750.	1.8	15
31	Dynamic epigenetic changes to <i>VHL</i> occur with sunitinib in metastatic clear cell renal cancer. <i>Oncotarget</i> , 2016, 7, 25241-25250.	1.8	14
32	Staphylococcal enterotoxin B influences the DNA methylation pattern in nasal polyp tissue: a preliminary study. <i>Allergy, Asthma and Clinical Immunology</i> , 2013, 9, 48.	2.0	13
33	Systemic Suppression of the Shoot Metabolism upon Rice Root Nematode Infection. <i>PLoS ONE</i> , 2014, 9, e106858.	2.5	13
34	DNA methylation profiling of primary neuroblastoma tumors using methyl-CpG-binding domain sequencing. <i>Scientific Data</i> , 2016, 3, 160004.	5.3	11
35	A genome-wide search for epigenetically regulated genes in zebra finch using MethylCap-seq and RNA-seq. <i>Scientific Reports</i> , 2016, 6, 20957.	3.3	9
36	<i>WRN</i> Promoter CpG Island Hypermethylation Does Not Predict More Favorable Outcomes for Patients with Metastatic Colorectal Cancer Treated with Irinotecan-Based Therapy. <i>Clinical Cancer Research</i> , 2016, 22, 4612-4622.	7.0	9

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37	SNP-guided identification of monoallelic DNA-methylation events from enrichment-based sequencing data. <i>Nucleic Acids Research</i> , 2014, 42, e157-e157.	14.5	6
38	Mining for viral fragments in methylation enriched sequencing data. <i>Frontiers in Genetics</i> , 2015, 6, 16.	2.3	5
39	Technical considerations in PCR-based assay design for diagnostic DNA methylation cancer biomarkers. <i>Clinical Epigenetics</i> , 2022, 14, 56.	4.1	5
40	Clinical utility study of confirms mdx for prostate cancer in a community urology practice.. <i>Journal of Clinical Oncology</i> , 2019, 37, 94-94.	1.6	3
41	Epigenetic sampling effects: nephrectomy modifies the clear cell renal cell cancer methylome. <i>Cellular Oncology (Dordrecht)</i> , 2017, 40, 293-297.	4.4	2
42	Clinically significant Prostate Cancer diagnosed using a urinary molecular biomarker-based risk score: two case reports. <i>BMC Urology</i> , 2019, 19, 124.	1.4	1
43	Cost-effectiveness of a two-gene urine biomarker assay in MRI strategies for the initial detection of prostate cancer.. <i>Journal of Clinical Oncology</i> , 2019, 37, 91-91.	1.6	1
44	Immune cell profiling of melanoma metastases from patients treated with TriMixDC-MEL dendritic cell therapy in combination with ipilimumab.. <i>Journal of Clinical Oncology</i> , 2017, 35, e21030-e21030.	1.6	0
45	Validation of a two-gene mRNA urine test for detection of high-grade prostate cancer in German men.. <i>Journal of Clinical Oncology</i> , 2019, 37, 96-96.	1.6	0